Figure 1 (SEQ ID NO:1)

```
   1 ATGAAGAAAC ATCTTAAAAC AGTTGCCTTG ACCCTCACTA CAGTATCGGT AGTCACCCAC
  61 AATCAGGAAG TTTTTAGTTT AGTCAAAGAG CCAATTCTTA AACAAACTCA AGCTTCTTCA
 121 TCGATTTCTG GCGCTGACTA CGCAGAAAGT AGCGGTAAAA GCAAGTTAAA GATTAATGAA
 181 ACTTCTGGCC CTGTTGATGA TACAGTCACT GACTTATTTT CGGATAAACG TACTACTCCT
 241 GAAAAAATAA AAGATAATCT TGCTAAAGGT CCGAGAGAAC AAGAGTTAAA GGCAGTAACA
 301 GAGAATACAG AATCAGAAAA GCAGATCACT TCTGGATCTC AACTAGAACA ATCAAAAGAG
 361 TCTCTTTCTT TAAATAAAAC AGTGCCATCA ACGTCTAATT GGGAGATTTG TGATTTTATT
 421 ACTAAGGGGA ATACCCTTGT TGGTCTTTCA AAATCAGGTG TTGAAAAGTT ATCTCAAACT
 481 GATCATCTCG TATTGCCTAG TCAAGCAGCA GATGGAACTC AATTGATACA AGTAGCTAGT
 541 TTTGCTTTTA CTCCAGATAA AAAGACGGCA ATTGCAGAAT ATACCAGTAG GGCTGGAGAA
 601 AATGGGAAA TAAGCCAACT AGATGTGGAT GGAAAAGAAA TTATTAACGA AGGTGAGGTT
 661 TTTAATTCTT ATCTACTAAA GAAGGTAACA ATCCCAACTG GTTATAAACA TATTGGTCAA
 721 GATGCTTTTG TGGACAATAA GAATATTGCT GAGGTTAATC TTCCTGAAAG CCTCGAGACT
 781 ATTTCTGACT ATGCTTTTGC TCACCTAGCT TTGAAACAGA TCGATTTGCC AGATAATTTA
 841 AAAGCGATTG GAGAATTAGC TTTTTTTGAT AATCAAATTA CAGGTAAACT TTCTTTGCCA
 901 CGTCAGTTAA TGCGATTAGC AGAACGTGCT TTTAAATCAA ACCATATCAA AACAATTGAG
 961 TTTAGAGGAA ATAGTCTAAA AGTGATAGGG GAAGCTAGTT TTCAAGATAA TGATCTGAGT
1021 CAACTAATGC TACCTGACGG TCTTGAAAAA ATAGAATCAG AAGCTTTTAC AGGAAATCCA
1081 GGAGATGATC ACTACAATAA CCGTGTTGTT TTGTGGACAA AATCTGGAAA AAATCCTTCT
1141 GGTCTTGCTA CTGAAAATAC CTATGTTAAT CCTGATAAGT CACTATGGCA GGAAAGTCCT
1201 GAGATTGATT ATACTAAATG GTTAGAGGAA GATTTTACCT ATCAAAAAAA TAGTGTTACA
1261 GGTTTTTCAA ATAAAGGCTT ACAAAAGTA AAACGTAATA AAAACTTAGA AATTCCAAAA
1321 CAGCACAATG GTGTTACTAT TACTGAAATT GGTGATAATG CTTTTCGCAA TGTTGATTTT
1381 CAAAATAAAA CTTTACGTAA ATATGATTTG GAAGAAGTAA AGCTTCCCTC AACTATTCGG
1441 AAAATAGGTG CTTTTGCTTT TCAATCTAAT AACTTGAAAT CTTTTGAAGC AAGTGACGAT
1501 TTAGAAGAGA TTAAAGAGGG AGCCTTTATG AATAATCGTA TTGAAACCTT GGAATTAAAA
1561 GATAAATTAG TTACTATTGG TGATGCGGCT TTCCATATTA ATCATATTTA TGCCATTGTT
1621 CTTCCAGAAT CTGTACAAGA AATAGGGCGT TCAGCATTTC GGCAAAATGG TGCAAATAAT
1681 CTTATTTTTA TGGGAAGTAA GGTTAAGACC TTAGGTGAGA TGGCATTTTT ATCAAATAGA
1741 CTTGAACATC TGGATCTTTC TGAGCAAAAA CAGTTAACAG AGATTCCTGT TCAAGCCTTT
1801 TCAGACAATG CCTTGAAAGA AGTATTATTA CCAGCATCAC TGAAAACGAT TCGAGAAGAA
1861 GCCTTCAAAA AGAATCATTT AAAACAACTG GAAGTGGCAT CTGCCTTGTC CCATATTGCT
1921 TTTAATGCTT TAGATGATAA TGATGGTGAT GAACAATTTG ATAATAAAGT GGTTGTTAAA
1981 ACGCATCATA ATTCCTACGC ACTAGCAGAT GGTGAGCATT TTATCGTTGA TCCAGATAAG
2041 TTATCTTCTA CAATAGTAGA CCTTGAAAAG ATTTTAAAAC TAATCGAAGG TTTAGATTAT
2101 TCTACATTAC GTCAGACTAC TCAAACTCAG TTTAGAGACA TGACTACTGC AGGTAAAGCG
2161 TTGTTGTCAA AATCTAACCT CCGACAAGGA GAAAAACAAA AATTCCTTCA AGAAGCACAA
2221 TTTTTCCTTG GCCGCGTTGA TTTGGATAAA GCCATAGCTA AAGCTGAGAA GGCTTTAGTG
2281 ACCAAGAAGG CAACAAAGAA TGGTCAGTTG CTTGAAAGAA GTATTAACAA AGCGGTATTA
2341 GCTTATAATA ATAGCGCTAT TAAAAAAGCT AATGTTAAGC GCTTGGAAAA AGAGTTAGAC
2401 TTGCTAACAG GATTAGTTGA GGGAAAAGGA CCATTAGCGC AAGCTACAAT GGTACAAGGA
2461 GTTTATTTAT TAAAGACGGC TTTGCCATTG CCAGAATATT ATATCGGATT GAACGTTTAT
2521 TTTGACAAGT CTGGAAAATT GATTTATGCA CTTGATATGA GTGATACTAT TGGCGAGGGA
2581 CAAAAAGACG CTTATGGTAA TCCTATATTA AATGTTGACG AGGATAATGA AGGTTATCAT
2641 GCCTTGGCAG TTGCCACTTT AGCTGATTAT GAGGGGCTCG ACATCAAAAC AATTTTAAAT
2701 AGTAAGCTTA GTCAATTAAC ATCTATTCGT CAGGTACCGA CTGCAGCCTA TCATAGAGCC
2761 GGTATTTTCC AAGCTATCCA AAATGCAGCG GCAGAAGCAG AGCAGTTATT GCCTAAACCA
2821 GGTACGCACT CTGAGAAGTC AAGCTCAAGT GAATCTGCTA ACTCTAAAGA TAGAGGATTG
2881 CAATCAAACC CAAAAACGAA TAGAGGACGA CACTCTGCAA TATTGCCTAG GACAGGGTCA
2941 AAAGGCAGCT TTGTCTATGG AATCTTAGGT TACACTAGCG TTGCTTTACT GTCACTAATA
3001 ACTGCTATAA AAAGAAAAA ATATTAA
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Figure 2 (SEQ ID NO:2)

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  1  MKKHLKTVAL  TLTTVSVVTH  NQEVFSLVKE  PILKQTQASS  SISGADYAES  SGKSKLKINE
 61  TSGPVDDTVT  DLFSDKRTTP  EKIKDNLAKG  PREQELKAVT  ENTESEKQIT  SGSQLEQSKE
121  SLSLNKTVPS  TSNWEICDFI  TKGNTLVGLS  KSGVEKLSQT  DHLVLPSQAA  DGTQLIQVAS
181  FAFTPDKKTA  IAEYTSRAGE  NGEISQLDVD  GKEIINEGEV  FNSYLLKKVT  IPTGYKHIGQ
241  DAFVDNKNIA  EVNLPESLET  ISDYAFAHLA  LKQIDLPDNL  KAIGELAFFD  NQITGKLSLP
301  RQLMRLAERA  FKSNHIKTIE  FRGNSLKVIG  EASFQDNDLS  QLMLPDGLEK  IESEAFTGNP
361  GDDHYNNRVV  LWTKSGKNPS  GLATENTYVN  PDKSLWQESP  EIDYTKWLEE  DFTYQKNSVT
421  GFSNKGLQKV  KRNKNLEIPK  QHNGVTITEI  GDNAFRNVDF  QNKTLRKYDL  EEVKLPSTIR
481  KIGAFAFQSN  NLKSFEASDD  LEEIKEGAFM  NNRIETLELK  DKLVTIGDAA  FHINHIYAIV
541  LPESVQEIGR  SAFRQNGANN  LIFMGSKVKT  LGEMAFLSNR  LEHLDLSEQK  QLTEIPVQAF
601  SDNALKEVLL  PASLKTIREE  AFKKNHLKQL  EVASALSHIA  FNALDDNDGD  EQFDNKVVVK
661  THHNSYALAD  GEHFIVDPDK  LSSTIVDLEK  ILKLIEGLDY  STLRQTTQTQ  FRDMTTAGKA
721  LLSKSNLRQG  EKQKFLQEAQ  FFLGRVDLDK  AIAKAEKALV  TKKATKNGQL  LERSINKAVL
781  AYNNSAIKKA  NVKRLEKELD  LLTGLVEGKG  PLAQATMVQG  VYLLKTPLPL  PEYYIGLNVY
841  FDKSGKLIYA  LDMSDTIGEG  QKDAYGNPIL  NVDEDNEGYH  ALAVATLADY  EGLDIKTILN
901  SKLSQLTSIR  QVPTAAYHRA  GIFQAIQNAA  AEAEQLLPKP  GTHSEKSSSS  ESANSKDRGL
961  QSNPKTNRGR  HSAILPRTGS  KGSFVYGILG  YTSVALLSLI  TAIKKKKY*
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Figure 3

Clustal W(1.4) multiple sequence alignment

7 Sequences Aligned.   Alignment Score = 118839
Gaps Inserted = 0   Conserved Identities = 936

Pairwise Alignment Mode: Fast
Pairwise Alignment Parameters:
    ktup = 1   Gap Penalty = 3   Top Diagonals = 5   Window Size = 5

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: blosum

Processing time: 12.9 seconds

```
Spy74_M3      1                                            DYAES      5
Spy70_M5      1                      LVKEPILKQTQASSSISGADYAES     24
Spy69_M6      1                            KQTQASSSISGADYAES     17
Spy68_M2      1                      LVKEPILKQTQASSSISGADYAES     24
Spy60_M1      1                      LVKEPILKQTQASSSISGADYAES     24
12357_M18     1                       VKEPILKQTQASSSISGADYAES     23
700294_M1     1  MKKHLKTVALTLTTVSVVTHNQEVFSLVKEPILKQTQASSSISGADYAES     50
                                                       *****


Spy74_M3      6  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT     55
Spy70_M5     25  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT     74
Spy69_M6     18  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT     67
Spy68_M2     25  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKTVT     74
Spy60_M1     25  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT     74
12357_M18    24  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT     73
700294_M1    51  SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    100
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Spy74_M3     56  ENTESEKQITSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS    105
Spy70_M5     75  ENTESEKQINSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS    124
Spy69_M6     68  ENTESEKQINSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS    117
Spy68_M2     75  ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS    124
Spy60_M1     75  ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS    124
12357_M18    74  ENTESEKQINSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS    123
700294_M1   101  ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS    150
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Spy74_M3    106  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    155
Spy70_M5    125  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
Spy69_M6    118  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    167
Spy68_M2    125  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
Spy60_M1    125  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
12357_M18   124  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    173
700294_M1   151  KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    200
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Spy74_M3     156  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    205
Spy70_M5     175  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    224
Spy69_M6     168  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    217
Spy68_M2     175  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    224
Spy60_M1     175  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    224
12357_M18    174  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    223
700294_M1    201  NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA    250
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Spy74_M3     206  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    255
Spy70_M5     225  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    274
Spy69_M6     218  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    267
Spy68_M2     225  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    274
Spy60_M1     225  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    274
12357_M18    224  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    273
700294_M1    251  EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP    300
                  *************************************************

Spy74_M3     256  RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    305
Spy70_M5     275  RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    324
Spy69_M6     268  RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    317
Spy68_M2     275  RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    324
Spy60_M1     275  RQLMRLAERAFKSNHIKTTEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    324
12357_M18    274  RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    323
700294_M1    301  RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK    350
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Spy74_M3     306  IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP    355
Spy70_M5     325  IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP    374
Spy69_M6     318  IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP    367
Spy68_M2     325  IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP    374
Spy60_M1     325  IESEAFTGNPGDDHYNNRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP    374
12357_M18    324  IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP    373
700294_M1    351  IESEAFTGNPGDDHYNNRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP    400
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Spy74_M3     356  EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI    405
Spy70_M5     375  EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI    424
Spy69_M6     368  EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI    417
Spy68_M2     375  EIDYTKWLEEDFTYQKNSVTGFSNKGLQKVKRNKNLEIPKQHNGVTITEI    424
Spy60_M1     375  EIDYTKWLEEDFTYQKNSVTGFSNKGLQKVKRNKNLEIPKQHNGVTITEI    424
12357_M18    374  EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI    423
700294_M1    401  EIDYTKWLEEDFTYQKNSVTGFSNKGLQKVKRNKNLEIPKQHNGVTITEI    450
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Spy74_M3     406  GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    455
Spy70_M5     425  GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    474
Spy69_M6     418  GDNAFRNVNFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    467
Spy68_M2     425  GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    474
Spy60_M1     425  GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    474
12357_M18    424  GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    473
700294_M1    451  GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD    500
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Spy74_M3    456 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR  505
Spy70_M5    475 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR  524
Spy69_M6    468 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR  517
Spy68_M2    475 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR  524
Spy60_M1    475 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR  524
12357_M18   474 LEEIKEGAFMNNRIETLELKDKLVTIQDAAFHINHIYAIVLPESVQEIGR  523
700294_M1   501 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR  550
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Spy74_M3    506 SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  555
Spy70_M5    525 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  574
Spy69_M6    518 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  567
Spy68_M2    525 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  574
Spy60_M1    525 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  574
12357_M18   524 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  573
700294_M1   551 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF  600
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Spy74_M3    556 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  605
Spy70_M5    575 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  624
Spy69_M6    568 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  617
Spy68_M2    575 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  624
Spy60_M1    575 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  624
12357_M18   574 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  623
700294_M1   601 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD  650
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Spy74_M3    606 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLIEGLDY  655
Spy70_M5    625 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY  674
Spy69_M6    618 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY  667
Spy68_M2    625 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMIDLEKILKLIEGLDY  674
Spy60_M1    625 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY  674
12357_M18   624 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY  673
700294_M1   651 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY  700
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Spy74_M3    656 STLRQTTQTQFRDMTTAGKALLSKSKLRQGEKQKFLQEAQFFLGRVDLDK  705
Spy70_M5    675 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK  724
Spy69_M6    668 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK  717
Spy68_M2    675 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK  724
Spy60_M1    675 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK  724
12357_M18   674 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK  723
700294_M1   701 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFPLGRVDLDK  750
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Spy74_M3    706 AIAKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD  755
Spy70_M5    725 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD  774
Spy69_M6    718 AIAKAEKALVTKKATKNGQLLERSINKAVSAYNNSAIKKANVKRLEKELD  767
Spy68_M2    725 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD  774
Spy60_M1    725 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD  774
12357_M18   724 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD  773
700294_M1   751 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD  800
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Spy74_M3    755 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  805
Spy70_M5    775 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  824
Spy69_M6    768 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  817
Spy68_M2    775 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  824
Spy60_M1    775 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  824
12357_M18   774 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  823
700294_M1   801 LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  850
                ***************************************************

Spy74_M3    806 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  855
Spy70_M5    825 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  874
Spy69_M6    818 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  867
Spy68_M2    825 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  874
Spy60_M1    825 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  874
12357_M18   824 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  873
700294_M1   851 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN  900
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Spy74_M3    856 SKLSQLTSIRQVPTAAYHRAGIPQAIQNAAAEAEQLLPKPGTHSEKSSSS  905
Spy70_M5    875 SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKAGTHSEKSSSS  924
Spy69_M6    868 SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS  917
Spy68_M2    875 SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS  924
Spy60_M1    875 SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS  924
12357_M18   874 SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS  923
700294_M1   901 SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS  950
                ****************************************** * *******

Spy74_M3    906 ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      951
Spy70_M5    925 ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      970
Spy69_M6    918 ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      963
Spy68_M2    925 ESANSKDRGLQSHPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL     971
Spy60_M1    925 ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL     971
12357_M18   924 ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      969
700294_M1   951 ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALLSLI 1000
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Spy74_M3    952              951
Spy70_M5    971              970
Spy69_M6    964              963
Spy68_M2    972              971
Spy60_M1    972              971
12357_M18   970              969
700294_M1  1001 TAIKKKKY 1008
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